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                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Roberts, J.A., Wyatt, P. and Whitelaw, C.
Signal transduction protein involved in plant dehiscence
Patent: WO 9949046-A 14 30-SEP-1999;
ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB);
WHITELAW CATHERINE (GB)
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Sequence 14 from Patent W09949046.
AX016311 GI:10041874
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/organism="Brassica napus" /db_xref="taxon:3708" 20._.430

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                                                                                                                                                               Brassica napus response regulator protein mRNA, complete cds AF057027
Whitelaw, C.A., Paul, W., Jenkins, E.S., Taylor, V.M. and Roberts, J.A
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                                                                                                                                                                                                                                                                                                            GGATGCTTGATGGATATATTTTATATTATGGAAACACACATAATAACGTCTAAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/protein_id="AAC6225.1"
/protein_id="AAC6225.1"
/db_xref="GI:3687688"
/translation="MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="up-regulated during pod development"
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AX016324
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TCACCTACACGTGTATTTGACACAAAAATCTGCATTTGTTGTGATATAGGGTTTCTCATA
                                 AACTCATGGATGCTTGATGGATATATTTTATA-----TTATGGAAACACACACATAATA
                                                                                                                              GCTCAACCATTGCTTGGAAAAACCCTTAACCAAGGCCAAGATCTTCCCGCTCATTAGCC
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                                                               ACCTCTTCGATGCTTGATGGATGAAGGCTCATTAATGTATCTATATTTTCAATCATGAAA
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AX016324
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Roberts, J.A., Wyatt, P. and Whitelaw, C.
Signal transduction protein involved in plant dehiscence
Patent: WO 9949046-A 27 30-SEP-1999;
ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PA
WHITELAW CATHERINE (GB)
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/db_xref="GI:10041880"
/db_xref="GI:10041880"
/translation="MATKSTGGTEKTKSIEVKKKLINVLIVDDDPLNRRLHEMIIKTI
/translation="MATKSTGGTEKTKSIEVKKKLINVLIVDDDPLNRRLHEMIIKTI
GGISQTAKNGEBAYILHENGEBASFDLTLIMDKEMPERDGVSTIKXLREMKGTSMIVGVT
SVADQEEERKAFMEAGLNHCLEKPLTKAKIFPLISHLEDA"
svadQEEERKAFMEAGLNHCLEKPLTKAKIFPLISHLEDA"
148 c 159 g 222 t 2 others
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/db_xref="taxon:3702"
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                                                                                                                                                                                                      ACAATGAAGAGGAACGTAAGGCTTTCATGGAAGCTGGACTTAACCATTGCTTGGCAAAAC
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                                                                                            ATGAATTGTCGCCACTACATATCTACATTATACAAATATGAAAAACACATATAATAACGT
                                                                                                                                                  ACAATGAAGAGGAGGGCGCAGGGCTTTCATGGAAGCTGGACTTAACCATTGCTTGGCAAAAC
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1 (bases 1 to 576)

1 (bases 1 to 576)

Roberts, J. A., Wyatt, P. and Whitelaw, C. Signal transduction protein involved in plant dehiscence Patent: WO 9949046-A 25 30-SEP-1999; ROBERTS JEREMY ALAN (GB); BIOGENMA UK LTD (GB); WYATT PAUL (GB); WHITELAW CATHERINE (GB)
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Brassica napus
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ilarity 75.4%;
Conservative
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-CTTTATCGTCCGTGATATATAATCATGTAAGTTGTTGCTTTAAGCTTA
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/db_xref="taxon:3708"
102 c 122 g 161
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Pred. No. 1.6e
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RESULT 5
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction programs including GRAIL (available by annowmous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Hitp://gnomic.stanford.edu/-chris/gENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/metpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity are named as 'unknown' proteins. Genes without protein programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAAATAATGAA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (24-GAN-2001) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Jan 24, 2001 this sequence version replaced gi:12280893.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin,X. and Kaul,S.

Direct Submission
Submitted (08-DEC-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 110804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC clone T6K12 is from Arabidopsis chromosome III and is near the molecular marker mi172.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,X., Kaui,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B., Wu,D., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bownan,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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complement(<1. .>1275)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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<2505. .>3566
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complement(join(<1. .100,188. .556,813. .1275))

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/note="hypothetical protein, 3' partial"
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GPTIAYDSGSEINKIMNLLPLVVRFSIENIVDLFPIALYGEEGPTGPKEKDNWEGDEM
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/gene="T6K12.3"
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join(<4235. .4346,5141.
/gene="T6K12.3"
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/gene="T6K12.2"
/note="hypothetical protein"
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    /protein_id="AAF26780.1"
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.11135,11282. .11403,
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Query Match Best Local S Matches 454 Local Similarity AATCGAAGATGGCAACAAAATCCACCGGAGGTACCGAGAAAACCAAGTCGATAGAAGTGA 30066 AATCGAAGATGGCAACAAAATCCATGGGAGATATCGAGAAAATAAAGAAGAAGAACTA---- 67 454; Conservative GFDALYLKMLACGIPTSVHLMWIPMSELSLQQQFLLVTRVVSRVFNALRKTQVVSNAK
DTVLEK RIN INDI IMMAVVFPV LEFI I PYQLRIRLGMAPPEEI EQTVGSTWYLQMQSE
AEMNEK SRINEDE QWELWELL RAS I YGGFVLYWFREELKRKVPRLLGYGGFREDDINKE
AEMNEK SRINEDE QWELWELL RAS I DGFVLYWFREELKRKVPRLLGYGGFREDDINKE
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LDGFEKQDGYVLMATTENHKQIDEALRRPGRMDRVFHLQSPTEMERERILHNAAEETM DRELVDLYDMRKVSEKTTLLRPIELKLVPMALESSAFRSKFLDTDELLSYVSWFATFS HIVPPWLRKTKVAKTMGKMLVNHLGLNLTKDDLENVVDLMEPYGQISNGIELLNPTVD WTRETKFPHAVWAAGRALITLLIPNFDVVENLWLEPSSWEGIGCTKITKVTSGGSAIG ESKKLQRDLQNRIRKRMKKFGEEKLFVQKTPEGEAVKGFPEAEVKMMFGEKEVVVPKA IQLHLRHGWKKWQEEAKADLKQKLLEDVDFGKQYIAQRQEQVLLDRDRVVSKTWYNED KSRWEMDPMAVPYAVSRKLIDSARIRHDYAVMYVALKGDDKEFYVDIKEYEMLFEKFG GLYRDMRRLRKERDLLMKRADKIVDEALSLKKQSEKLLRKGAREKMEKLEESVDIMES EYNKIWERIDEIDDIILKKETTTLSFGVRELIFIERECVELVKSFNRELNQKSFESVP ESSITKLSRSEIKQELVNAQRKHLEQMILPNVLELEEVDPFFDRDSVDFSLRIKKRLE /translation="MDFISASSLSSPFSTQLSPIYLSSGIVSLKPRHRVKNRNFGSRE
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Roberts, J.A., Wyatt, P. and Whitelaw, C.
Signal transduction protein involved in plant dehiscence
Patent: WO 9949046-A 23 30-SEP-1999;
ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAN
WHITELAW CATHERINE (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GAMACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGAT 120
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33; Conserv
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Dorner, F., Scheiflinger, F. and Falkner, F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified
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/translation="MATTSTSTGDIKKTKSVEVKKKLNVLIVDDDTVIRKLHENIIKS
IGGISQTAKNGSEAVNIHRDGNA"
256 c 264 g 576 t 16 others
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Vibrio fischeri RscS (rscS) gene,
AF319618
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Euprymna scolopes by Vibrio fischeri
J. Bacteriol. 183 (3), 835-842 (2001)
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Vibrio fischeri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Visick, K.L. and S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Visick, K.L. and Skoufos, L.M.
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QNWYSNITVIYDLESLLKLKYFKEYTIHTIFLLEKQLTNUNGNYEDKYLTSQLTLHR
TLPKEIALSDTAINDSDETSLPNYIKLKKITESKPKEQSIDSTVKQTLTKQNAYWITQ
SETIKTQLFITTLFLLCCIALYEYIKLKKITESKPKEQSIDSTVKQTLTKQNAYWITQ
SETIKTQLFITTLFLLCCIALYEYIKLKKITESKPKEQSIDSTVKQTLTKQNAYWITQ
SETIKTQLFITTLFLLCCIALYEYIKLKKITESKPKEQSIDSTVKAKLALYAEYA
HDAIFILDKQGRLTWINGSYSALSGNYLEDIESKDLPSILOLKIKHANIIILLQSILE
TGTSISFELTNHHKDGTILFWLTYLLEDHEKDLPSILOLKIKALSGHKLLESGH
LLFLLNEILDFATNSHLELTPLNGILGNAQIIESNIKDKEQHKQIKKILIDKINN
LIFULINGILDFSKIEQNKLELNHASFYFVDIIEPITNTYLSVCENKGLKFIIDKINN
EIVFIGDKERIRQIIFNANYKFTHEGSITLNFSHTLTGKKGQAVQIKIKDTGVGI
RENRIKHIFEPYIQAEASTTRQYGGTGLGLATVKQLTDIMROYISVSSEGKGSCFTL
VLPLDITKSKQLKDNDALLPSGOSKSINFIPAMNULSIIIAEKLKISTVLFAYTAN
HAAIIAENGKVALDKLKETHFDLIIMNNHAPVADGILATKIIREKLKISTVLFAYTAN
HOOVALMANTITTULGENDALTOKAGATTA
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KRPSKYKLSDDALTEAETKLTSTQDTCGTDSETTCVFLQSFTDTSEENITETTAFER
KDIKSTREVAHSIKGMASNESASRLIKTATSTELCAKKKNMEKLEDVQQLINLLKINI
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/db_xref="taxon:668"
782. .3565
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/product="RscS"
/product="RscS"
/protein_id="AAG60694.1"
/db_xref="G1:12620414"
/translation="MKNQLLRYSLITIITCTLIIIYLMLTRNHPVKQYQRAYLTPSHN
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/gene="rscs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 19, 2001 this sequence version replaced gi:17384505.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate prinary accession numbers given
in the feature table with their source databases: Em. EMBL; SW:,
SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
thttp://www.sanger.ac.uk/Projects/C.elegans/wormpen This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCAAGGACAAGATCATCCCTCTCATTAACCAACTCATGGATGC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
http://www.sanger.ac.uk/HGP/Chr9
RR11-17718 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                         sections only once, except for a short overlap.
The true left end of clone RP11-515J13 is at 109753 in this
                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-17718 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-DEC-2001) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                             /clone_lib="RPCI-11.1"
19899 c 20215 g 37062
                                                                                                                                                                        /chromosome="9"
                                                                                                                                                /clone="RP11-17718"
8.5%;
Score 51.4;
Pred. No. 0.
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DB 9;
.021;
                     Length 111752;
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Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,
Gardner, M.J., Tettelin, H., Carucci, D.J., Kupiii, C., Pederson, J.,
Koonin, E. V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,
Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,
Smith, H.O., Fraser, C.M., Hoffman, S. L. et al.
Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AE001420 AE001362
AE001420.1 GI:3845287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-NOV-1998) The Institute for Genomic Medical Center Drive, Rockville, MD 20814, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner, M.
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/translation="mikyinkskalllrkmstvknmsksnqltkeifmalkektsllq
keklyiefyeemiclsmletscoelfyfflmyksridnyvbelkvybekgegskgtnnom
lnnndxtfsfstdokgfinkeeggeekknefnanyeaukkybpebgsyglulpybyk
vefykhiielidslaadvvyrhsigvykrndkynfvtvlfnnlktyeknvfhhefsfa
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/protein_id="AAC71956.1"
/db_xref="GI:3845289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Plasmodium
/db_xref="taxon:5833"
                                                                                                                                                                                            /note="predicted by GlimmerM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PFB0830w"
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    393
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GCATTATTTTGATGAACGATGTCATCCAACCTTTTTGGTCGGTACTTTTCAACCCACGGA 7545
                                                                          GCAGGGCTTTCATGGAAGCTGGACTTAACCATTGCTTGGCAAAACCGTTAACCAAGGACA 392
                                                                                                                                     Similarity
                                                                                                                                                                                                                  6057
                                                                                                                  Conservative
                                                                                                                                                                                                                                             /gene="PFB0840w"
7534 . .8526
/gene="PFB0840w"
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SRCSCYRFQSIPINIKKEKLLYICQNENIDIVDALEKIIET/TEGDLERAVSIIQLCS
CINTKITINSVLDVSGLPSDNIVYKILDACKMKDLKLVEKTVGDIIEDGFDVAXIFKS
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9688. .10611
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complement(11963..14386)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYYIMNLIPEKEHNLFSLFKVFNEIKTMHPKNISVLYFYDRIQRTYIVINKFFEDVPQ
FLLCLLYITLNGKDKFIIFNMLYSIIYFVINAIYHGLNYPLMGTLNLFFSTYLLELYI
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52.6%;
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Pred. No. 0
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PFMAL13P2_3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 114; Conserv
1-193488
Birren B., Lin:
"Homo sapiens of
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                56551 TGAAAGCAGGATAACAGCAGAGCAAGCTTTAAATCACCCTTGGTTCCAAGAAAATTAAAA 56492
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                                                                Eukaryota;
Eutheria;
                                                                                                                           Homo sapiens
25 unordered
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                                                                                   Homo sapiens (human)
                                                                                                       HTG; HTGS_DRAFT; HTGS_PHASE1
                                                                                                                                                           15-DEC-1999
28-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                  GCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAATCATGTAAGT 559
                                                                                                                                                                                                                                                                                                                                                                                        ATTITATATIATGGAAACACACATAATAACGTCTAAGTGTGTATGTATGCATAGATACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name
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           Linton L., Nusbaum C., ens chromosome 4, clone
                                                                          Metazoa;
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300001
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                                                               Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  DNA;
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           Lander E.;
RP11-402C9";
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                                                                          Mammalia;
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 1877768 bases at least Q40
Consensus quality: 187917 bases at least Q20
Consensus quality: 187917 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 191088; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on May 26, 2000 this sequence version replaced gi:6649474. All repeats were identified using RepeatMasker: Smit, A.F. A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
1-193488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tirrell A., Vassilio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1340 1439: gap of 1339 bp in length 1340 1439: gap of 100 bp 100 length 2664 2763: gap of 100 bp 2764 4211: contig of 1244 bp in length 4212 4311: gap of 100 bp 100 length 5619 5718: gap of 100 bp 5719 6795: contig of 1307 bp in length 6796 6895: gap of 100 bp 5719 6895: gap of 100 bp 100 length 6896 11378: contig of 1077 bp in length 6896 11378: contig of 2392 bp in length 11279 11278: gap of 100 bp 100 length 11279 11278: gap of 100 bp 11279 13748: contig of 2470 bp in length 113749 13848: gap of 100 bp 13949 13948: gap of 100 bp 110 length 13949 13948: gap of 100 bp 100 length 13949 13948: gap of 100 bp 100 length 13949 13949: contig of 2470 bp in length 13949 13949: contig of 2901 bp in length 13949 13949: contig of 1810 bp in length 13949 14939: contig of 1810 bp in length 14949: contig of 1
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17950 20794: cont
20795 20894: gap of
20895 23299: cont
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78 36477: gap of 10
78 45186: contig of 8
87 45286: gap of 10
53168: contig of 7
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23299: c
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53269. .62404
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1. .1339
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2 (bases) to 198509)
Waterston,R.H.
Direct Submission
Submitted (25-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Feb 8, 2002 this sequence version replaced gi:18370048.
      Sequencing vector: M13; 35%
Sequencing vector: plasmid; 65%
                                                                                         Drafting center: WIBR
                                                                                                          Center project name:
                                                                                                                         Contact: submissions@watson.wustl.edu
                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198509)
Waterston, R. H.
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62505. .73127
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94982. .107947
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73228. .82813
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159694. .193488
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136476. .159593
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91; Conserv
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Insert size: 197809; sum-of-contigs
Quality coverage: 13.78 in Q20 bases; agarose-fp
Quality coverage: 13.76 in Q20 bases; sum-of-contigs
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/chromosome="4"
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1737. .6279
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13179: contig of 2502
13279: gap of unknown
198509: contig of 18523
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1507: gap of unknown length
2836: contig of 1329 bp in length
4936: gap of unknown length
4636: contig of 1700 bp in length
4736: gap of unknown length
6279: contig of 1543 bp in length
6379: gap of unknown length
7570: contig of 1191 bp in length
7570: gap of unknown length
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TITLE
                                   JOURNAL
                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                            151498 bp DNA
Homo sapiens chromosome 3 clone RP11-90B15,
AC099331 AC073441
AC099331.2 GI:18652541
Direct Submission
Submitted (09-NOV-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 151498)
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 151498)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saephimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1324)
Roberts, J. A., Wyatt, P. and Whitelaw, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal transduction protein involved in plant dehiscence Patent: WO 9949046-A 29 30-SEP-1999; ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB); WHITELAW CATHERINE (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29
AX016326
                                                            2 (bases 1 to 151498)
Kaul, R.K., Olson, M.V., Raymond, C. and
                                                                                                                        Direct Submission
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/db_xref="taxon:3702"
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/db_xref="G1:10041882"
/translation="MATKSTGGTEKTKSIEVKKKLINVLIVDDDPLNRRLHECHQ" .
214 c 182 g 467 t 1 others
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/note="unnamed protein product"
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71.38;
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                                                                Haugen, E.D
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Quality coverage: 9.0x in Q20 bases; sum-of-contigs
Insert size: 149290; sum-of-contigs
Consensus quality: 151498 bases at least Q20
494 bases at least
408 bases at least
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rminator Big Dye
Dye-terminator ET; 92% c
vector: plasmid; 68% of
328
Summary Statistics
Center clone name: RP11-90B15 (bc0621)
Center project name: chr-3
Project Information
Drafting Center: BCM
Contact: uwgchtgs@u.washington.edu
Web site: http://www.genome.washington.edu
Center Code: UWGC
Center: University of Washington Genome Center
Genome Center
On Feb 12, 2002 this sequence version replaced gi:16874865.
5, Seattle, WA 98195, USA
Submitted (12-FEB-2002) Genome Center, University of Washington,
Direct Submission
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Overlapping Sequences:

5': Mapping in progress 3': RP11-613N24 (UWGC:bc0491) AC099557

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality - 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

SeqDerMap This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. 6382 512 970 HindIII FngrPrnt <800 6463 SeqDerMap 8580 5474 2067 BglII FngrPrnt 5794 2050 8813 SeqDerMap 6481 8696 ECORI FngrPrnt 6581 <800 ďď

<800

6597

6842

5809

17594 17727 3302 3325 1952 1917 5889 5961 1006 1006 5653 5690 1462 1474 5122 5184 11891 1917 276 <800 10522 10095	2050 527 <800 1721 1006 12425 1 4195 652 783 437 2050 5996	5491 5794 7737 7651 74 <800 16863 17203 3542 3693 2501 2550 4519 4717 5219 5184 924 923 6649 6581 5553 5992 764 <800 1495 1474 2623 2550	783 2020 13846 3842 1161 490 4399 5591 4399 11077 3549 902 1474 6995 1604 6862 783 435
Search completed: November 7, 2002, 14:05:25 Job time: 2373 secs	OY 439 TATTITATATITAGGAAACACACATAATAACGTCTAAGGTGTATGCATAGATACT 498	/Cione=_In=TP11-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Inb==RPI1-90B15" //Cione=_Index=	6792 6880 882 907 434 <800 1331 1316 1753 1741 2550 2406 1166 1161 1166 1161 11753 1741 2550 2406 11753 1741 2550 2406 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 1741 11753 175

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Listing first 45 summaries
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A. thaliana DZZATI
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Pinus
  Brassica response
Brassica napus DZ2
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involved in plant le sterile plants									plant; DZ2 gene; protein; ss.						n immune sys	immune sys	orkimmine s	ically treat	Human immune syste Human immune/haema	ır suppre	immune	immune	Human immune/haema	immune	Human immune/haema	Human immune syste	ם מ	Nucleotide sequenc	Human immune syste	Drosophila melanog	Tumour suppressor Human endometriosi	Genomic DNA sequen	Tumour suppressor	eri		Chemically pretrea	thaliana DZ2AT uman immune/haem

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Best Local
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Brassica response
                                                              AAZ22977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                    10-JAN-2000
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                                                                                                                                                                                                              TATGTATGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGT
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                                                                                                                  CTACC
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                                                                                                                                                                                                                                             GGATGCTTGATGGATATATTTTATATTATGGAAACACACATAATAACGTCTAAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Fig 1;
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                    (first entry)
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regulator
                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 605; DB 20; 100.0%; Pred. No. 3.9e-159;
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protein
                                                              ВP
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DZ2
DNA sequence
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The pressequence represents the B. napus DZ2 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A nucleic acid encoding dehiscence, useful for p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 605 BP; 198 A; 101 C; 140 G; 166 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-580449/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1999;
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CCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCAT
                                                                                                                                                                               GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAA
                                                                                                                                                                                                                                                                                                                                                                           CCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGAT
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                                                            CCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCAT
                                                                                                                                                     GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAA
                                                                                                                                                                                                                                                 GGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig
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oilseed rape; response regulator protein; ss
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Pred. No. 3.9e-159;
0; Mismatches 0;
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9908-013945 9908-013946 9908-013946 9908-013976 9908-013976 9908-013976 9908-013976 9908-014083 9908-014082 9908-0142154 9908-014205 9908-014205 9908-014205 9908-014207 9908-014207 9908-014207 9908-0144085 9908-014432 9908-014432 9908-014433 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014524 9908-014531 9908-014531 9908-014531 9908-014531 9908-014531 9908-014531 9908-014531 9908-014531	9US-0137724 9US-0138094 9US-0138840 9US-01389119 9US-0139453 9US-0139453 9US-0139453 9US-0139453 9US-0139453

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         50.3%;
Score 304.2; DB 21
Pred. No. 4.2e-75;
0; Mismatches 133;
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        Wyatt P,
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                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                            AAZ22978;
                         (BIOG-) BIOGEMMA UK LTD
                                           20-MAR-1998;
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         Roberts JA, Whitelaw C;
                                                                                                                                                         DZ2AT3 cDNA sequence.
                                                                                                                                                                         (first entry)
                                           98GB-0006113
                                                           99WO-GB00905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A nucleic acid encoding dehiscence, useful for r
                                    AAC47939 standard;
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                                                                                                                                                                                         TCTATGTTTGATTTATTTTCTTATCGTCCGAGGTAAAATCATGCAAGTCATTTCTTTTGG
                                                                                                                                                                                                             -----AGGGTTCTTTATCGTCCGTGATATATATCATGTAAGTTGTTGTTGTTTAAG
                                                                                                                                                                                                                                                            TCACCTACACGTGTATTTGACACAAAAATCTGCATTTGTTGATATAGGGTTTCTCATA
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Pred. No. 3.3
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3.3e-73;
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                         TAATCATCCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGC
                                              AGAAGATCATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAG
                                                                              ------ACGTGTTGATCGTCGATGATGATCACCACTAAACCTTATAATTCATG
                TGATCCTCCACCGTGACGGCGAAGCATCTTTCGACCTTATTCTAATGGATAAGGAAATGC
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62; Conservative
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Pred. No. 4.6e-73;
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(first entry) haliana DNA fragme: assay; genetic maj ification; signal; hway; promoter; te haliana. 2000EP-0301439. 99US-0125788 99US-0125788 99US-0125788 99US-0126264 99US-0126264 99US-0132486 99US-0130077, 99US-0130510, 99US-0132486 99US-0132487 99US-0132487 99US-0132486 99US-0134218 99US-0134218 99US-0134370, 99US-0134370, 99US-0135124 99US-0135124 99US-0135124 99US-0135124 99US-0135124 99US-0135124 99US-0135124 99US-0135124	
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Best Local
                                                                                                                                                                                                                                                                                   Signal transduction protein; dehiscence; male sterile plant; DZ2B gene; shatter resistance; oilseed rape; response regulator protein; ss.
                                                                                                                                                                                                                                                                                                                                                           Brassica response regulator protein DZ2B cDNA sequence
(BIOG-) BIOGEMMA UK LTD.
                                                20-MAR-1998;
                                                                                           22-MAR-1999;
                                                                                                                                            30-SEP-1999
                                                                                                                                                                                                                                        Brassica napus
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990S-0157117 990S-0157753 990S-0158029 990S-0158029 990S-0158232 990S-0158293 990S-0159294 990S-0159294 990S-0159295 990S-0159295 990S-0159330

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Best Local Sim
Matches 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed trape (Brassica napus). The present sequence represents the B. napus DZ2B cDNA sequence.
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             AAZ22975;
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                                        AAZ22975 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 576 BP; 188 A; 102 C; 122 G; 161 T; 3 other;
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Pred. No. 5e-71;
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Best Local :
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           Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modifiplant cell signalling; modulation; transgenic plant; pathogen; environmental change; development; cell proliferation; different elongation; survival; disease resistance; nutrient metabolism;
                                                                                                                                                                                                                                                                                           1628
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                                                                              Pinus radiata cell signalling involved polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                                                1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica napus
                                                                                                          27-NOV-2000
                                                                                                                                                                 AAA79325
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1716 BP; 604 A; 256 C; 264 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-580449/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wyatt P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOG-) BIOGEMMA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09949046-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2000
                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                           AAATAAAGAAGAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTC 110
                                                                                                                                                                                                                                    CAGTGAACATCCACCGCGACGGC 1710
                                                                                                                                                                                                                                                               CAGTAATCATCCACCGTGACGGC 193
                                                                                                                                                                                                                                                                                        AAGTGAAGAAGAAACTTAACGTGTTGATCGTTGATGATGATACAGTAATTCGTAAACTTC 1627
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Fig 5; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY42644
                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DZ2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0006113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB00905
                                                                                                                                                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; dehiscence; male sterile plant; DZ2B
oilseed rape; response regulator protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitelaw C;
                                                                                                                                                                1656
                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 106.2;
; Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
                                                                                                                                                                 뭐
                      Monterey pine; plant; modification; transgenic plant; pathogen; growth; cell proliferation; differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partial coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                       23;
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Indels Length

0;

Gaps

0

1687

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NO:63

protein; dehiscence; male sterile plant; DZ2AT3; oilseed rape; response regulator protein;

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RESULT 10
AAZ22979
ID AAZ22
XX
AC AAZ22
XX
AC AAZ22
XX
DT 10-JA
XX
DE A. th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and protein sequences isolated from eucalyptus (Eucalyptus grandis) or the pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynuclectide and protein sequences sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and cevelopment of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other corgans providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear way.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    A. thaliana DZ2AT3
                                  10-JAN-2000
                                                                 AAZ22979;
                                                                                             AAZ22979 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1656 BP; 514 A; 283 C; 400 G; 459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 58; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                  611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pinus radiata
                                                                                                                                                                          728
                                                                                                                                                                                                       252
                                                                                                                                                                                                                                      671
                                                                                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                132
                                                                                                                                                                                                                                                                                                                                                       551 TCTTGCTCGTGGAAGACACACAAATCAACAGAATAATTTTCGGGAGGGTGCTTCAAAGCC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                   72 TGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGATCATCAAAGCGA 131
                                                                                                                                                                                                CGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCA 310
                                                                                                                                                                                                                                                                                            TTAATCTTTACTGTGAAGAAGCTGAGAATGGGAAAGTAGCAGTGGACTATTTCAAGCAGG
                                                                                                                                                                   AGGCAACAAGGCAACTGAGATCAATGGGAGTCAAGACACCCATTGTTGCACTTACAGCA 786
                                                                                                                                                                                                                                                             GCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCCGAGAGGGATGGTGTTT
                                                                                                                                                                                                                                                                                                                         TTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAATCATCCACCGTGACG 191
                                                                                                                                                                                                                               133;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0228986
990S-0162866
   promoter region and
                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  55.68;
                                                                                             1324
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58.2;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
   partial
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1656;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                            670
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AAK73166/
XX
XX
AC AAK7
XX
XX
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DT 06-N
XX
XX
DT U06-N
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Huma
XX
KW Huma
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KW cyto
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Homo
OS Homo
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XX
PN WO20
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                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                            1312
                                                                                                                                                                                                                                                                                                                                                                                                                   1192
              WO200157182-A2
                                            Homo sapiens
                                                                       cytostatic; gene
                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                  AAK73166;
                                                                                                                                                                                                               166/c
AAK73166 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal transduction shatter resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY42648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wyatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1999;
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                                                                                                                                                                                                                                                                                                                        114
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                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                         AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                            1313
                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the promoter region and a partial coding region of A. thaliana DZ2AT3 gene.
                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                   Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1252 AGAAGAAACTAATCAACGTGTTGATCGTCGATGATCATTATAACCGTAGACTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1324 BP; 460 A; 214 C; 182 G; 467 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-580449/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 11; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOG-) BIOGEMMA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 AATCGAAGATGGCAACAAAATCCATGGGAGAATATCGAGAAAATAAAGAAGAAACTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCGAAGATGGCAACAAAATCCACCGGAGGTACCGAGAAAACCAAGTCGATAGAAGTGA 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-0006113
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therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATG 113
                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitelaw C;
                                                                                                                                                                                                                                                                  19965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.
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Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                      SEQ ID NO:27978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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14-AUG 2000
12-AUG 2000
12-AUG 2000
22-AUG 2000
22-AUG 2000
23-AUG 2000
23-AUG 2000
01-SEP 2000
01-SEP
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17-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
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11-JUL-2000
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2001WO-US01354
 29-SEP-2000
22-SEP-2000
22-SEP-2000
22-CCT-2000
22-CCT-2000
22-CCT-2000
22-CCT-2000
23-CCT-2000
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23-CCT-2000
20-CCT-2000
20-CCT
WPI;
2001-483426/52
                       Barash SC,
                                                                     2000US-0236368

2000US-0236369

2000US-0236370

2000US-0237039

2000US-0237039

2000US-0237039

2000US-0237039

2000US-0241785

2000US-0241786

2000US-0241820

2000US-0244617

2000US-0244617

2000US-0246476

2000US-0246526

2000US-0249211

2000US-0249211

2000US-0249216

2000US-0251938

2000US-0251869

2000US-0251869

2000US-0251989

2000US-0251989

2000US-0251999
                                               GENOME
                                                 SCI INC
                       Ruben
                       SM;
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RESULT 12
AAS445453
ID AAS45
XX AAS45
XX AAS45
XX CAAS45
XX GAT1
XX GA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CP proteins and polynucleotides may be used in the prevention diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For CP example, they may be used to treat disorders associated with decreased CP expression by rectifying mutations or deletions in a patient's genome CP that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CP polynucleotides may be used to produce the secreted (I), by inserting CP concers and cancer metastases of haematopoietic acids into a host cell and culturing the cell to express the CP protein. (I) proteins and polynucleotides may be used to prevent, CP diagnose and treat immune/haematopoietic-related diseases, especially CP cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CP cancers and cancer metastases of haematopoietic antigen genomic CP sequences from the present invention. AAK54912 to AAK54950 and AAM82169 CP represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
   15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle; human; CpG dinucleotide; cytosine methylation, human immunodeficiency virus; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4661
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                                                                                                                                                                                                                                                                                                                                                                                                         graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS45453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS45453 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                              15-MAR-2001;
                                                                                                                                                                                                         20-SEP-2001
                                                                                                                                                                                                                                                                WO200168911-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemically pretreated complementary DNA associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547
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                                                                                                                                                                                                                                                                                                                                                                                primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTCATATATATTATATATATTTTCATATATATATATTTA 4558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
   ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                              2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 4699 A; 5296 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.6; DB Pred. No. 0.022; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 4465 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; HIV; aging; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cycle #79
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В QV

4665

375 AACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCATGGATGCTTGATGGA 434

0

digestive system

02-AUG-2001

WO200155314-A2

Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds.

RESULT 13 AAK89374/c

AAK89374 standard;

DNA;

32206

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05-NOV-2001

(first entry) system

digestive

antigen

genomic

sequence

SEQ

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NO:

appendicitis; chronic colit

colitis;

AAK89374;

В ΩV 밁 Š

4785

495

4725

435

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555

4845 TAGGGTGATTAATATATATATATATTTTATAATT 4879

TAAGTTGTTGCTTTAAGCTTATAAAATATTTAAAT

TACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATAATCATG AAGTTTTAGTAAAGAGAAAAAATATTATTGTATATATAGGAGTTAGATGTAATTTATAGA 4724

4844 554 4784

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Matches
                                Query Match
Best Local :
                                                                                                                                                                             Sequences AAS45206-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HTV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arterioscolerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with cell cycle
                                                                                                                            Sequence 9515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 158; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-)
      109;
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS
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      Conservative
                                                                                                                            2719 A; 220 C; 1904 G; 4672 T; 0 other;
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                             7.5%;
50.7%;
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   0;
                                Score 45.4;
Pred. No. 0.
   Mismatches
                                DB,
   106;
                                                              22;
   Indels
                                                           Length
                                                                 9515;
0
   Gaps
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31-JAN-2000
24-FEB-2000
24-FEB-2000
10-MAR-2000
11-MAR-2000
11-MAR-2000
11-MAR-2000
11-JUL-2000
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11-JUL-2000
11-AUG-2000
11-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
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2000US-0186350
2000US-019974
2000US-019974
2000US-0199123
2000US-0199123
2000US-0199123
2000US-02151886
2000US-0216647
2000US-0216647
2000US-0217496
2000US-0217497
2000US-0217497
2000US-0217497
2000US-0217497
2000US-0220963
2000US-0225964
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2000US-0225266
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2000US-0225275
2000US-0225275
2000US-0225275
2000US-02257575
2000US-0225758
2000US-0231243
2000US-0231413
2000US-0231414
2000US-0231414
2000US-0232080
2000US-0232981
2000US-0232399
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2000US-0232399
2000US-0232401
2000US-0232401
2000US-0232401
2000US-0233063
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2000US-023433
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2000US-023433
2000US-023583
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2000US-0229509.
2000US-0229513.
2000US-0230437.
2000US-0230438.
2000US-0231242.
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2000US-0229344.
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 17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-2000
02-CCT-2000
02-CCT-2000
02-CCT-2000
01-CCT-2000
20-CCT-2000
01-NOV-2000
08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
Polynucleotides encoding digestive system antigens, useful for
                                                                                                                                                                                                                                                                                     17-NOV-2000;
7-NOV-2000;
1-DFC
                                                                                    ( HUMA - )
                              2001-502630/55
                                                      CA,
                                                                                    HUMAN
                                                                                                             2000US-0236370
2000US-02376370
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0231809
2000US-02411787
2000US-0241808
2000US-0241808
2000US-02446178
2000US-02464774
2000US-02464774
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2000US-0246610
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2000US-0249211
2000US-0249218
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2000US-0251988
2000US-0251988
2000US-0251988
2000US-0251988
2000US-0251988
                                                                                    GENOME
                                                       sc,
                                                                                     SCI
                                                         SM;
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RESULT 14
AAV839
ID AAV83
XX AAV83
XX O3-MA
XX Yeast
XX Yeast
XX Yeast
XX Homo
DE HC-CC
XX HOMO
DE HC-CC
XX 19-NC
PN W0985
XX HOMO
PN W0985
XX 13-MA
XX 13-MA
XX 13-MA
XX 13-MA
XX 12-NC
PD 13-MA
XX 13-M
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Best Local S
Matches 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis ulcerative colitis. The present sequence is a genomic DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
  The present sequence represents the chromosome 10, 10q25.2 region. This
                                                                                                                                                      New isolated nucleic acid comprising neocentromere sequences eukaryotic chromosome - used to produce replicable, segregati artificial chromosomes that can carry large amounts of DNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases \cdot
                                                                                Claim 8; Fig 6;
                                                                                                                                                                                                                                                                   WPI; 1999-009773/01.
                                                                                                                                                                                                                                                                                                                     Cancilla MR,
                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-1997;
13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09851790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HC-contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32206 BP; 9503 A; 5480 C; 7017 G; 10206 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19~NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATGTGTATATGTGTATATATATGTGTATATATATACGTGT 22034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAGATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from normal human chromosome 10q25.2 region.
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                                                                                                                                                                                                                                                                                                                  Choo K,
                                                                                                                                                                                                                                                                                                                                                                    OPERATIONS PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                      97AU-0008791.
97AU-0006784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-AU00352
                                                                           540pp;
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                                                                                English
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Pred. No. 0.
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HC-contig derived from normal human region can be naturally mutated to
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                                                                                                                                                            segregating of DNA for
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC produce an unusual chromosomal marker referred to as mardel(10). The CC mardel(10) marker is mitotically stable and contains a functional CC neocentromere at a location regarded as non-centromeric. This cc neocentromere maps to q25.2 on chromosome 10. The specification describes CC nucleic acid sequences derived from a cukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in CC a compatible cell, of replicating, acting as extra-chromosomal element CC construct artificial chromosomes for use in gene therapy comprising a CC construct artificial chromosomes for use in gene therapy comprising a CC construct artificial chromosomes can propagate in human cells and CC carry large amounts of DNA (e.g. therapeutic genes), and, being CC extra-chromosomal, they are not mutagenic. The artificial chromosomes CC are also useful for generation of transgenic plants and animals, in CC production of proteins and to make diagnostic reagents, e.g. for CC expression of cytokines, receptors and growth factors, or to increase CC used for functional and structural analysis of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
16-WAR-2000;
17-WAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                            04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                         31-JAN-2000;
                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                    cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                     Human; immune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                             WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK76447 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80595 BP;
                          2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
                                                                                     2000US-0190076.
2000US-0198123.
2000US-0205515.
                                                                                                                                            2000US-0180628.
2000US-0184664.
2000US-0186350.
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                                                                                                                                                                                                                                                                                                                                                    haematopoietic;
                                                                                                                                                                                                                                                                                                                                    therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 4445
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54.28;
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Pred. No. 0.
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14-AUG-2000
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23-AUG-2000
01-SEP-2000
    14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
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14-JUL-2000;
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20000S-023934414
20000S-023931243
       01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own produce the secreted (I). By inserting polynucleotides may be used to produce the secreted (I) by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic useful for preventing, diagnosing and/or treating metastasis -
                                                                                                                                                                                                                                                                                                                    metastasis
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                                                                                                                                                                                                                                                                                                                                       antigen
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Search completed: November 7, 2002, 12:30:12 Tob time: 291 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4445 BP; 1164 A; 1222 C; 1054 G; 1005 T; 0 other;
                                                                         737 TATATATTTTT 748
                                                                                                             519 TTTAGGGTTCTT 530
                                                                                                                                                677 CACATATACACATATATGCGTATATATATATATATATACGTATATATGTGTATATGTATA 736
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ster than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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(without alignments)
3161.878 Million cell updates/sec
Sequence 63, Appli
Sequence 14, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 70, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 70, Appli
Sequence 26, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 11, Appli
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                                                                               RESULT 2
US-08-232-463-14/c
; Sequence 14, Application
; Patent No. 5670367
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US-09-228-986-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-228-986-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: 100/1020
CURRENT FILING LATION NUMBER: US/09/228,986
CURRENT FILING DATE: 199-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 63
SEQ ID NO 63
LENGTH: 1656
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000
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Best Local Sim.
Matches 133;
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 GENERAL INFORMATION:
APPLICANT: DORNER, FAPPLICANT: SCHEIFLIN
APPLICANT: FALKNER,
APPLICANT: FALKNER,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Applica
Patent No. 6359198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728
                                                                                                                                                                                                                      252
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33; Conservative
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                 DORNER, F.
SCHEIFLINGER,
FALKNER, F. G.
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US-08-477-500-1
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US-08-454-097-1
US-08-453-866-1
US-08-185-359-1
US-08-950-022-11
US-08-950-022-11
US-08-950-022-11
US-08-950-544-4
US-08-950-544-4
US-08-950-544-4
US-08-950-544-4
US-08-950-544-4
US-08-951-209-3
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Pred. No. 1.1e-07;
0; Mismatches 103;
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US-09-078-294-3
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US-08-486-013-7
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US-08-42-268-7
US-09-015-968-7
US-09-015-968-7
US-09-078-294-4
US-09-078-294-3
US-09-078-294-3
US-09-078-294-3
US-09-078-294-3
US-09-078-294-3
US-09-078-294-3
US-09-078-294-3
US-09-078-078-34-1
US-09-078-078-784-1
US-09-078-786-1
US-09-255-984-1

Minimum Maximum

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length:

20000000000

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hits satisfying

chosen parameters:

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued_Patents_NA:*

1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,

/cgn2_6/ptodata/1/ina/5A_COMB.seq: *
/cgn2_6/ptodata/1/ina/5B_COMB.seq: *
/cgn2_6/ptodata/1/ina/6B_COMB.seq: *
/cgn2_6/ptodata/1/ina/6B_COMB.seq: *
/cgn2_6/ptodata/1/ina/backfiles1.seq: *

Title: Perfect score:

US-09-646-679-14 605

nucleic

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nucleic search,

using

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model

GenCore version Copyright (c) 1993 - 2002

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November

2002, 10:50:27

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

383533 seqs, 122816752 residues

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US-08-232-463-14
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)83-4109
TELEPAX: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELETAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: DECLE SEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: si-
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                             1425
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1000
CITY: Alexandria
                                                                                               1125
                                                                                                                                                               1185
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                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
 421
                                                                361
                                                                                                                                                                                              241
                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      61 GAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCACGAGCAGAATCGAAGATGGCAACAAATCCATGGGAGATATCGAGAAAATAAAGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                        CCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGCTTGATGGATATA 438
                                                         CCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCAT 420
                                                                                                                                                                                         GGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGG 300
                                                                                                                                                                                                                                                                                         CATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAATCAT 180
                             GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAA 360
                                                                                                                                                                                                                        h 8.9%; Score 54; DB 1; Length 7218; Similarity 7.5%; Pred. No. 3.1e-06; 33; Conservative 220; Mismatches 185; Indels
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; TYPE: DNA ; ORGANISM: Nucleotide sequence of NC-contig US-09-078-294-4
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US-09-078-294-4
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; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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US-09-078-294-3
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEO ID NOS: 29
CORMINER DATE: DATE: 1998-05-13
NUMBER OF SEO ID NOS: 29
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09078294 Patent No. 6265211 GENERAL INFORMATION:
                                                                                                                                                                      Query Match
-- rocal Similarity
Conser
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cannilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                 15605 ATAAATATGTATATGTGTATATAGACATAAATATGTATATATGTGTATATAGACATAA 15664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Davies Col
15665 ATATGTATATATGTGTATATAGACATAAATATGTGTATATAGTGTATATAGACATAAATAT 15724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15708 ATATGTATATATGTGTATATAGACATAAATATGTATATGTGTATAT 15755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15648 ATAAATATGTATATGTGTATATAGACATAAATATGTATATATGTGTATATAGACATAA 15707
                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                        550 TCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 ATAGATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.2%;
                               ATACTTGCATGTGTGTGTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATAATCAT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Conservative
                                                                                                                                                                                                                                                                                                                     80246
                                                                                                                                                                        Conservative
                                                                                                                                                                                        7.3%;
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Pred. No. 0.0063;
0; Mismatches 75;
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Pred. No. 0.0037;
O: Mismatches 77;
                                                                                                                                                                                                              Length 80246;
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                                                                                                                                                                      Indels
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US-09-381-862-3
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US-09-381-862-3/c
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/381,862
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1997-71077
APPLICATION NUMBER: JP 1997-71077
FILING DATE: 25-MAR-1997
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 624590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15725 GTATATGTGTGTATATAGACATAAATATGTATATGTGTGTAT 15768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25 MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/:
FILING DATE: 23 MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
2814 GGACGTGAAGGGGTTGATTTGGCATTGGCTTTGAAGCCAGATGTTTTGGTTATGGATCTA 2755
                                                                        2874 GGACTCAAGAGTTTTTTGAATTTACAAGCTGATATTGATGTCGTTGGTGAGGCCTCTAAT
                                                                                                                                                   2934 GAGATGACGATGAGTAAGATAAAAGTGATATTGGTCGATGATCATGAAATGGTCCGCATG 2875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                             554 GTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                      47 GAGAAAATAAAGAAGAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATA 106
                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pyogenes
STRAIN: Clinical Isolate SP-14-1
                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                    GAGGCAGTAATCATCCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60606
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: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5014 base pairs
                                                                                                                                                                                                                            6.6%;
ilarity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuhisa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ueyama, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keshi, Hiroyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abe, Kanako
                                                                                                                                                                                                                                                                                                                                                                                                     linear
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PROBES FOR THE DIAGNOSIS OF INFECTIONS
CAUSED BY STREPTOCOCCUS PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT/JP98/01288
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Pred. No. 0.031;
0; Mismatches 195; Indels
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RESULT 6
US-08-486-013-70
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Patent No. 5731149
GENERAL INFORMATION:
Query Match 6.6%;
Best Local Similarity 45.6%;
Matches 140; Conservative
                                                                                                                                                                                                     TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: US 07/
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18 NOV-12
APPLICATION NUMBER: US
                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2637
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Selsted, michael E. APPLICANT: Ouellette, Andre J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2754 GTGATGCCAGAGTTAGGCGGTGTTGAGGCAACTTTAGAAGTTCTAAAAAAATGGAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIILE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
IIILE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347
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                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGCAGGAGCGAAGGGTTATATGTTAAAAACATCGAGTGCGGCTGAAATTTTAAATGCC 2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGCTGGACTTAACCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTC 406
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                                                                                                                                                             2551 base pairs
                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1994
                                                                                                                        single
                                                                                                                                                                                                                           535-8949
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                                                                                                                                                                                                                                                                                                                                                                                      US 07/889,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/342,268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  07/930,649
  0;
                                                                                                                                                                                                                                                                                     P-UC 1206
Score 39.8; DB 1;
Pred. No. 0.027;
0; Mismatches 167;
                                    Length 2551;
    Indels
  0;
Gaps
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298 TGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACT 357

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<u>В</u>
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US-08-482-279-70
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   Query Match
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                                                                                                                                                                                                                                                             FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AuG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                         TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Selste
APPLICANT: Ouelle
                                                                                                                                                                            NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: Of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 CACTTAC 309
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                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/342,268 FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                          LENGTH:
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California
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4370 La Jolla Village Drive, Suite
                                                                                                         2551 base pairs
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                                                                                                                                                                                                                  P-UC 1206
 Score 39.8;
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Length 2551;
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RESULT 8
US-08-342-268-70
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                                                                 TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                              CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930

FILING DATE: 14-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/889

FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

REFERENCE MORKET NUMBER: 3-17
                                               SEQUENCE CHARACTERISTICS:
                                                                                                                   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ouellett
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                    TELEPHONE:
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 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGGATGCTTGATGGATATATTTTATTATTATGGAAACACACATAATAACGTCTAAGT
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                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                               2551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selsted, Michael E.
Ouellette, Andre J.
NVENTION: Ancibiotic Cryptdin Peptides and Methods
NVENTION: of Their Use
                                                                                     (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                    (619)
single
                                                                                    535-8949
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0; Mismatches 1
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                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015 040

FILING DATE:

CLASSTETT
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Best Local Sim
Matches 140;
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GENERAL INFORMATION:
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                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 14-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION UNMBER: US 08/482,279
APPLICATION NUMBER: US 08/482,279
                                                                                                                                                         FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                               FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
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                 NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                    APPLICATION NUMBER:
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4370 La Jolla Village Drive, Suite
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 NUMBER:
                                                                                                                                        US 07/930,649
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P-UC 3003
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RESULT 10
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Best Local s
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APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 2551 base pairs
APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                  CLASSIFICATION: PRIOR APPLICATION DATA:
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 US 08/342,268
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Pred. No. 0
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0.027;
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PRIOR APPLICATION DATA:

18-NOV-1994

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; ORGANISM: Drosophila virilis US-09-031-563-26
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US-09-031-563-26
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REFERENCE/DOCKET NUMBER: 9-UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9909
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272
CIPDENTIA
     Best Loc
Matches
                                                                                                                    SEQ ID NO 26
LENGTH: 4586
                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09031563A Patent No. 6022708
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Best Local Similarity 45.6%;
Matches 140; Conservative
                                    Query Match
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/031,563A CURRENT FILING DATE: 1998-02-26
                                                                                                                                                       NUMBER OF SEQ ID
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LENGTH: 2551 base pairs
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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     Local Similarity nes 89; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TCTTGACTGATAGATCTAACCCTACAGAGAGATTCAAGTGGTCTTGTCCCCATTGAACAAT
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STRANDEDNESS: single
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26-MAY-1992
                  52.0%;
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 Score 39.8; DB 3;
Pred. No. 0.034;
0; Mismatches 82;
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                                  Length 4586;
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 3
Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                             FILE REFERENCE: Davies Co.
                                                                  TYPE: DNA ORGANISM: Nucleotide sequence of HC-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                    15306 GTGTGTATATGTACATACATACATACATAAATA 15270
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                                                                                                                       LENGTH: 80595
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                  6.4%;
52.9%;
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                  Score 38.6; DB Pred. No. 0.23;
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US-08-629-643A-5
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                                                                                                  Matches
                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                2563 CTGCATATATATATATATATATATATATATATATATATGTGTGTGTGTGTGTGTGTGTGT 2622
                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/629,643A FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
APILICATION NUMBER: 08/629,643
APTIORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, N. A. TITLE OF INVENTION: I
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 486 ATGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTAT 533
                                                              426 CTTGATGGATATATTTTATATTATGGAAACACACATAATAACGTCTAAGTGTGTATGT 485
                                                                                                                                                                                 NAME/KEY: mat_peptide
LOCATIO: 650...371
OTHER INFORMATION: Join 650..730, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-359-3263
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                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Viksnins, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREET: P. O. Box 2938
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linear
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Pred. No. 0.17;
0; Mismatches 44;
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Search completed: November Job time: 293 secs
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-280-799-1
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Best Local Similarity 59.3%;
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: MCKAY, Robert
TITLE OF INVENTION: ARTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
TITLE OF INVENTION: TRANSDUCTION
FILE REFERENCE: ISPH-0340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09280799 Patent No. 6136603
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/280,799
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               7, 2002, 12:40:54
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Pred. No. 0.17;
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2002
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BE822715
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 CNS06MZ3
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(without alignments)
4826.039 Million cell updates/sec
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Compugen Ltd
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                                        AW278862 sf99f11.y
BE822715 GM700018B
BE454895 HVSMEh009
BE602512 HVSMEh009
BE602512 HVSMEh009
BM373897 EBMA03_SQ
BI509132 BB170013B
AQ488569 RPC1-11-2
BM368320 EBed01_SQ
BM415113 OP20184 M
ALIZ2093 Tetradom
AZ640886 1M0503E11
AZ009832 RPCI-23-3
BH516724 BOGIH80TR
BM373028 EBma04_SQ
AL406117 T7 end of
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VERSION
KEYWORDS
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AW278862
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DEFINITION
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AUTHORS
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JOURNAL
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ALIGNMENTS

I (bases 1 to 376)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., I wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., I., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., I., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Public, Soybean, EST Project Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, 1 AW278862 AW278862.1 AW278862 376 bp mRNA linear EST 02-DEC-2001 sf99f11.yl Gm-c1019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1019-4394 5' similar to TR:082445 082445 RESPONSE REGULATOR PROTEIN. ;, mRNA sequence. Email: est@watson.wustl.edu
Trace considered overall poor quality This clone is available
through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway
Huntsville, AL 35801 For further information call: (800)-533-4363
or contact via email: ccu@resgen.com
Seq primer: -40Rp from Gibco
High quality sequence stop: 1. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae; Glycine max Tel: 314 286 1800 Fax: 314 286 1810 quality sequence stop: 1.
Location/Qualifiers /organism="Glycine max" GI:6667411 MO 63108, USA Bowers , Schurk Beck,C Khanna

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62 AAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGATC 121
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Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., C
Erpedding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other_ESTs: AW278862 corresponding to Gm-c1019-4294 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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GM700018B10H9 Gm-r1070 Glycine max cDNA clone Gm-r1070-7289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sai I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I restriction site of the psporTI vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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Site_2: Sal I; This cDNA library was constructed from me
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the Life Technologies pSuperScript cDNA library
the Life Technologies pSuperScript cDNA library
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1019-4294"
/clone_lib="Gm-c1019"
/tissue_type="immature seed coats of greenhouse grown plants"
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Pred. No. 9
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9.5e-08;
                                                                           Retzel,E., Khanna,A., Coryell,V
Pardinas,J., Liu,L. and Lewin,H.
Soybean (NSF 9872565)
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                                                     AAATACGAAAATTTATGGAAGCGGGACTGAATGACTACCATGAGAAACCCTTGAACAATT
                                                                                                       AGCGCAGGGCTTTCATGGAAGCTGGACTTAACCATTGCTTGGCAAAACCGTTAACCAAGG
                                                                                                                                                            GCTCAATGGGCATTGGTAGCATGATTGTTGGTGTATCATCACGCTGT---ACGGAAGCAG
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DEFINITION

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146 182 80

320

ACCESSION VERSION

KEYWORDS

ORGANISM

COMMENT

274 389 329

334

d.

TITLE AUTHORS REFERENCE

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150 CAGCGAATAACGGTGAGGAGGCAGTAATCATCCACCGTGACGGCGGCTCATCTTTTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                 90 ATCCACTAAACCTTATAATTCATGAGAAGATCATCAAAGCGATTGGGGGGTATTTCACAGA 149
                                                                                  TTATCCTAATGGATAAAGAAATGCCCGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAA
                                                                                                                                                                         GAGTNGAAAATGGCCAAGAAGCAGTGGACATTCA---TTGCCATNGACAAAGATTTGACC
                                                                                                                                                                                                                                                                                                                                               ATAAAATCNNNNGAAAGATTCATCAAAAGCTGTTGGAGAGTGTTGGAATGAAAAATCAAG
TGATTCTCATGGACATGGATATGCCCCATCATGAATGGCATTGAGGCAACAAAGGAACTTC
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Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ystems.com web site:www.genomesystems.com
Seq primer: 5'.TTTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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/Clone='Taxon: 944'
/Clone='The library Gm-r1070'
set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from inmature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked to form library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.

Reracking was performed by Genome Systems, St. Louis, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.

Reracking was performed by Genome Systems, St. Louis, http://www.tfe.uiuc.edu/biotech/keck.html. Note: The Mintersity of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID of 'OTHER EST'. Sp. 179 to the Systems clone ID 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., 1, Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On Jul 26, 2000 this sequence version replaced gi:13189622.
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HVSMED0095H05f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEb0095H05f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute Clemson University
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        109
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Location/Qualifiers
                                                                                                                                                                                            /notes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; /notes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; /lotes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chol)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Cates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or sequence analysis see
see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 133 c 182 g 78 t
                                                                                                             sequence analysis see

http://www.genome.clemson.edu/projects/barley. To or

http://www.genome.clemson.edu/orders

this clone see http://www.genome.clemson.edu/orders
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HVcDNA0009 (5 to 45 DAP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="5-45 DAP Spike"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000 this sequence version replaced gi:13189622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one-"HVSMEh0095H05f"
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Best Local Sim
Matches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCGGGCTTGCGTAGCGGCCAT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCCAGGGGCTTTCATGGAAGCTGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCGTGCGGGACGGCGCGCGGGGCGCGTATGATCTCATCCTCACGGACAAGCAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCACCGTGACGGCGCTC---ATCTTTTGACCTTATCCTAATGGATAAAGAAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGAAGATCAGGGTGCTCCTAATGGAGGACCAGGAGATCCACAGGGTTGTGGCGAGAGC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCATGGATGCTTGATGGATAT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCGACGACTTCACGCCCAAGCCGCTGACCAAGGAGAAGCTGGGCAACATTCTCTCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE602512 732 bp mRNA linear EST 22-OCT-2001
HVSMEh0099H16f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099H16f.
                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare
                                                                                                                                                                                                 Email: rwing@clemson.edu
Total hq bases = 508
                                                                                                                                                                                                                                                                                                                                                                                     On Aug 21, 2000 t
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                              primer: AATTAACCCTCACTAAAGGG
                                                                                                                             quality sequence stop:
Location/Qualifiers
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                        /cultivar="Morex"
/db_xref="taxon:4513"
  /clone="HVSMEh0099H16f"
                                                                            /organism≔"Hordeum vulgare"
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Pred. No. 0.
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                                                                                                                                                                                                                                                              GTTCGGGCTTGCGTAGCGGCCAT 412
                                                                                                                                                                                                                                                                                                                  ACTCATGGATGCTTGATGGATAT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCATGGACGCCACGAGGCGACGAGGCAGATCCGGGCGATGGGGGGTGACCACGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAGATCAGGGTGCTCCTAGTGGAGGACCAGGAGATCCACAGGGTTGTGGCGAGAGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTAACCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCGCCGTG---TCCAGCGACAGCCTCCCGTCGGATGTCCAGGCCTTCATCGCCGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGCTGAGGGCGGCCGGTGTGGAGGCGGACGAGGCCAAGAACGGCGCCGAGGCGGTGCG 152
                                                                                                                                                                                                                                                                                                                                                                     AGCCGACGACTTCACGCCCAAGCCGCTGACCAAGGAGGAGGAGCTGGGCAACATTCTCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189;
                                                вм373897.1
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39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phree value 20 or above a contains a minimum of 100 bases of pared value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 177 c 226 g 147 t 27 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence analysis see
http://www.genome.clemson.edu/projects/barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP)"
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/lab_host="SOLR"
                      GI:18117287
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49.3<del>8</del>;
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y EBma03 library Hordeum
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Pterygota; ; Apoidea;
                                                                                                                                                BI509132 266 bp mRNA linear EST
BB170013B10E07 Bee Brain Normalized/Subtracted Library,
mellifera cDNA clone BB170013B10E07 5', mRNA sequence.
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Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
                                      Apis mellifera
Eukaryota; Met
                                                                                                              BI509132.1
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Hordeum vulgare
                                                                        honeybee
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Fax: 00 44 1382 562426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: psporm1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psporm1. Derived from maternal tissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4513"
/clone="EBma03_SQ003_A24"
/clone=1ib="IGF Barley EBma03 library"
/clone_type="Maternal tissue"
/dev_stage="8 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Optic"
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata
Apidae; Apis.
                                                                                                              GI:15359506
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Pred. No. 0.12
0; Mismatches
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                                                                                                                                                                                                             TGTGTATGTATGCATAGATACTTGCATGTGTGTGTTTAGAATTTAGGGTTCTTTATCGT 536
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                                                                                                                                                                                                                                                               CCGTGATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATA 590
                                                                                                                                                                                                                                                                                                                 Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: generobidife.uiuc.edu
This research was funded by the University of Illinois Critical
This research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behavior in the Honey Bee
Unpublished (2001)
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Whitfield,C.W., Soares,B.,
Smoller,D. and Robinson,G.
An Expressed Sequence Tag
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DNA sequence.
AQ488569
                                                 AQ488569
RPCI-11-243N4.TJ
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BACKWARD: ATTAACCCTCACTAAAG
INsert Length: 266 Std Erro
Plate: BB170013B10 row: E co
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Drime: AGCGGATAACAATTTCACACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the soares laboratory and it was constructed and normalized as described by Bonaldo, M.F. Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
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/clone_lib="Bee Brain Normalized/Subtracted
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/db_xref="taxon:7460"
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/strain="mixed strains of
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Pred. No. 0.37;
D; Mismatches 79;
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RPCI-11-243N4,
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                      Hordeum vulgare
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                EBed01_SQ002_N02_R IGF Barley clone EBed01_SQ002_N02 5', mRI
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Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Other_GSSs: RPCI-11-243N4.TV
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(bases 1 to 442)
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/note="Vector: pBACe3.6; Site_1:
/note="V
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/clone="RPCI-11-243N4"
/clone_lib="RPCI-11"
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/db_xref="GDB:7593243"
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yta; Liliopsida;
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Invergowrie, Dundee, DD2
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                               1 (bases 1 to 1745)
Heer, J. Sosinski, B., Pokrzywa, R.M., Warry, A. and Opp
Mixed Stage EST's from Globodera pallida, the potato
Unpublished (2001)
Contact: Opperman, C
                                                                                                                     Globodera pallida.
Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                                                                                                               1745 bp mRNA linear EST 28-JI OP20184 Mixed Stage EST's from Globodera pallida, the potato nematode Globodera pallida cDNA, mRNA sequence BM415113
                     Center for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwaugh@scri.sari.ac.uk
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/clone="ib="10F Barley EBed01 library"
/tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
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Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acanthomorpha; Acument Tetraodon.
Tetraodontidae; Tetraodon.
1 (bases 1 to 1024)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Roest-Crollius, H., Jaillon, C., Roest-Crollius, H., Jaillon, C., Parameter, C., Roest-Crollius, H., Jaillon, C., Roest-Crollius, H., Lander, Roest-Cr
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Tetraodon nigroviridis genome survey sequence T7 end of clone
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                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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Tel: 919.515.6699
Fax: 919.515.9500
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GT11-11PCN_R_H05_GT11-11_R_044.ab1
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1 ACR-Rothamsted."

2 5 0 547 t 25 others
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/db_xref="taxon:36090"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre C'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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/db_xxef="taxon:99883"
/clone="184002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ301735 S25 bp DNA linear GSS 23-Gm_UMb001_050_A08F Glycine max genomic clones containing regene analogs from UMN Soybean BAC Library (pECSBAC4 EcoRI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1099
                                                                                                                                                                                                           495 Borlaug Hall, 1991 Upper Buford Circ Tel: 612 625 2225 Fax: 612 625 9728 Email: neviny&tc.umn.edu Sequence on contig Gm_NBSDH8_ctg_b near
                                                                                                                                                                                                                                                                                                                                               BAC end sequences from analogs (RGAs)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            max genomic, DNA sequence. AZ301735
                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Young Nevin D
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
                                                                                                                                                                                                                                                                                                                                                                        Penuela, S., Larson, K., Foster-Hartnett, D. and
                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 525)
Penuela, S., Larson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ301735.1
                                                                                                                                                                                              NBSDH8
                                                                                                                                                                   primer: M13F
ss: BAC ends.
/tissue_type="cotyledon leaves"
/dev_stage="cotyledon stage"
/note="Vector: pECSBAC4; Site_1
                                              resistance gene analogs (pECSBAC4 ECORI)"
                                                                                        /organism="Glycine max"
/cultivar="Faribault"
/db_xref="taxon:3847"
                                                                         /clone_lib="Glycine max
                                                                                                                                                   Location/Qualifiers
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Muri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0503 row: E column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10\mathrm{kb} plasmid inserts
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0503E11"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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Pred. No. 1.5;
0; Mismatches 89;
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                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 GTTCTTTATCGTCCGTGATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATT
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                                                                 Unpublished (1999)
Other_GSSs: RPCI-23-324H4.TV
Other_GSSs: RPCI-23-324H4.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MT
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120;
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 to 610)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                 ,B., Levins,M.,
and Fraser,C.M.
Mouse BAC End S
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ009832
RPCI-23-324H4.TJ RPCI-23 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ00983:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
                                                   Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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                                                                                                                                                                                                                                                                                         Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M.,
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TITLE
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                             1 (bases 1 to 853)
Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shortgun sequencing of Brassica oleracea
Unpublished (2001)
Other.GSSs: BOGIH80TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 324 row: H column: 4
Seg primer: SP6
                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq_primer: TR
                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea.
Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends.
                                 Seq primer: TR
Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                      BH516724.1 GI:17724814
                                                                                                                     Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                      2 Medical Center Drive, Rockville, 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "B6 c 85 g 195 t 1 others
Location/Qualifiers
1. .853
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/clone="RPCI-23-324H4"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
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1.7;
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BOGIH80, DNA
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/organism="Brassica oleracea"

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                                                                                                              GGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACT 417
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                                                                                                                                                                                                                                                                                                                                                                                              /strain="TO1000DH3"
/db_xref="taxon:3712"
/dlone="BOGIHB0"
/clone=lib="BOGI"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 154 c 145 g 286 t
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